PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/356,575*

DATE: 08/02/1999
TIME: 14:04:52

OIPE

INPUT SET: S32736.raw

> **This Raw Listing contains the General Information Section and those Sequences containing ERRORS.**

see item 3 on Error Summary Sheet

```
 1                                SEQUENCE LISTING          Does Not Comply
 2                                                    Corrected Diskette Needed
 3      (1)     General Information:
 4                      (i)   APPLICANT: FALLAUX et al.
 5                            (ii)   TITLE OF INVENTION: PACKAGING SYSTEMS
 6                            (iii)  NUMBER OF SEQUENCES: (22)  20 shown (see
 7                            (iv)   CORRESPONDENCE ADDRESS:            last
 8                      (A) ADDRESSEE: RAE-VENTER LAW GROUP, P.C.       pages)
 9                      (B) STREET: 260 SHERIDAN AVENUE, PO BOX 60039
10                      (C) CITY: PALO ALTO
11                                       (D) STATE: CALIFORNIA
12                      (E) COUNTRY: USA
13                      (F) ZIP: 94306
14                      (v)   COMPUTER READABLE FORM:
15                      (A) MEDIUM TYPE: Floppy disk
16                      (B) COMPUTER: IBM PC compatible
17                      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
18                      (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
19                            (vi)   CURRENT APPLICATION DATA:
20                      (A) APPLICATION NUMBER: US 08/793,170   move down-there
21                      (B) FILING DATE: 25-MAR-1997                belong
22                      (C) CLASSIFICATION:                         under
23                            (vii)   PRIOR APPLICATION DATA:      PRIOR
24                      (A) APPLICATION NUMBER: WO 97/00326        APP DATA.
25                      (B) FILING DATE: 14-JUN-1996
26                            (vii)   PRIOR APPLICATION DATA:
27                      (A) APPLICATION NUMBER: EP 95201728.3
28                      (B) FILING DATE: 26-JUN-1995          use upper-case
29                            (vii)   PRIOR APPLICATION DATA:   I, not
30                      (A) APPLICATION NUMBER: EP 95201611.1   lower-case
31                      (B) FILING DATE: 15-JUN-1995              i
32                            (viii)   ATTORNEY/AGENT INFORMATION:
33                      (A) NAME: TURNER, ALLEN C.
34                      (B) REGISTRATION NUMBER: 33,041
35                      (C) REFERENCE/DOCKET NUMBER: 3935US
36                            (ix)   TELECOMMUNICATION INFORMATION:
37                      (A) TELEPHONE: (801)532-1922
38                      (B) TELEFAX: (801)531-9168
39                      (C) TELEX: N/A
```

ERRORED SEQUENCES FOLLOW:

Suggestion: Consult Sequence Rules for valid format.

INPUT SET: S32736.raw

```
-->   40   (2) INFORMATION FOR SEQ ID NO:1:        [use numeral "1",
      41              (i) SEQUENCE CHARACTERISTICS:   not lower-case "l"]
-->   42                      (A) LENGTH: 21 base pairs
      43   (all text           (B) TYPE: nucleic acid
      44    must be            (C) STRANDEDNESS: single
      45   invisible)          (D) TOPOLOGY: linear              use numeral "1"
      46              (ii) MOLECULE TYPE: other nucleic acid
      47
      48   DO NOT USE TAB CODES       <-- move over    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
                                                       CGTGTAGTGT ATTTATACCC G

      49   (2) INFORMATION FOR SEQ ID NO:2:
      50              (i) SEQUENCE CHARACTERISTICS:
-->   51                      (A) LENGTH: 21 base pairs        CRF program needs
      52                      (B) TYPE: nucleic acid           to "see" all bases;
      53                      (C) STRANDEDNESS: single         that is why (A)LENGTH:
      54                      (D) TOPOLOGY: linear             lines are in bold print.
      55              (ii) MOLECULE TYPE: other nucleic acid
      56                           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
      57                                           <--    TCGTCACTGG GTGGAAAGCC A

      58   (2) INFORMATION FOR SEQ ID NO:3:
      59              (i) SEQUENCE CHARACTERISTICS:
-->   60                      (A) LENGTH: 21 base pairs
      61                      (B) TYPE: nucleic acid
      62                      (C) STRANDEDNESS: single
      63                      (D) TOPOLOGY: linear
      64              (ii) MOLECULE TYPE: other nucleic acid
      65                           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
      66                                           <--    TACCCGCCGT CCTAAAATGG C

      67   (2) INFORMATION FOR SEQ ID NO:4:
      68              (i) SEQUENCE CHARACTERISTICS:
-->   69                      (A) LENGTH: 20 base pairs
      70                      (B) TYPE: nucleic acid
      71                      (C) STRANDEDNESS: single
      72                      (D) TOPOLOGY: linear
      73              (ii) MOLECULE TYPE: other nucleic acid
      74                           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
      75                                           <--    TGGACTTGAG CTGTAAACGC

      76   (2) INFORMATION FOR SEQ ID NO:5:
      77              (i) SEQUENCE CHARACTERISTICS:
-->   78                      (A) LENGTH: 21 base pairs
      79                      (B) TYPE: nucleic acid
      80                      (C) STRANDEDNESS: single
      81                      (D) TOPOLOGY: linear
      82              (ii) MOLECULE TYPE: other nucleic acid
      83                           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
      84                                           <--    GCCTCCATGG AGGTCAGATG T

      85   (2) INFORMATION FOR SEQ ID NO:6:
      86              (i) SEQUENCE CHARACTERISTICS:
-->   87                      (A) LENGTH: 20 base pairs
```

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/356,575*

INPUT SET: S32736.raw

```
88                        (B) TYPE: nucleic acid
89                        (C) STRANDEDNESS: single
90                        (D) TOPOLOGY: linear
91              (ii) MOLECULE TYPE: other nucleic acid
92                        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
93                                          GCTTGAGCCC GAGACATGTC
```

```
94      (2) INFORMATION FOR SEQ ID NO:7:
95              (i) SEQUENCE CHARACTERISTICS:
-->  96                   (A) LENGTH: 24 base pairs
97                        (B) TYPE: nucleic acid
98                        (C) STRANDEDNESS: single
99                        (D) TOPOLOGY: linear
100             (ii) MOLECULE TYPE: other nucleic acid
101                       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
102                                         CCCCTCGAGC TCAATCTGTA T
```

```
103     (2) INFORMATION FOR SEQ ID NO:8:
104             (i) SEQUENCE CHARACTERISTICS:
--> 105                   (A) LENGTH: 27 base pairs
106                       (B) TYPE: nucleic acid
107                       (C) STRANDEDNESS: single
108                       (D) TOPOLOGY: linear
109             (ii) MOLECULE TYPE: other nucleic acid
110                       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
111                                         GGGGGATCCG AACTTGTTTA T
```

```
112     (2) INFORMATION FOR SEQ ID NO:9:
113                       (i) SEQUENCE CHARACTERISTICS:
--> 114             (A) LENGTH: 25 base pairs
115                   (B) TYPE: nucleic acid
116                   (C) STRANDEDNESS: single
117                   (D) TOPOLOGY: linear
118             (ii) MOLECULE TYPE: other nucleic acid
119                       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
120                                         GGGAGATCTA GACATGATAA G
```

```
121     (2) INFORMATION FOR SEQ ID NO:10:
122             (i) SEQUENCE CHARACTERISTICS:
--> 123                   (A) LENGTH: 27 base pairs
124                       (B) TYPE: nucleic acid
125                       (C) STRANDEDNESS: single
126                       (D) TOPOLOGY: linear
127             (ii) MOLECULE TYPE: other nucleic acid
--> 128     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
129                                         GGGAGATCTG TACTGAAATG T
```

use numeral 1

```
130     (2) INFORMATION FOR SEQ ID NO:11:
131                       (i) SEQUENCE CHARACTERISTICS:
--> 132             (A) LENGTH: 24 base pairs
133                   (B) TYPE: nucleic acid
134                   (C) STRANDEDNESS: single
135                   (D) TOPOLOGY: linear
```

INPUT SET: S32736.raw

```
136                (ii) MOLECULE TYPE: other nucleic acid
137                          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
138                                              GGAGGCTGCA GTCTCCAACG G
```

```
139      (2) INFORMATION FOR SEQ ID NO:12:
140                (i) SEQUENCE CHARACTERISTICS:
-->  141                     (A) LENGTH: 27 base pairs
142                          (B) TYPE: nucleic acid
143                          (C) STRANDEDNESS: single
144                          (D) TOPOLOGY: linear
145                (ii) MOLECULE TYPE: other nucleic acid
146                          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
147                                              GGGGGATCCT CAAATCGTCA C
```

```
148      (2) INFORMATION FOR SEQ ID NO:13:
149                (i) SEQUENCE CHARACTERISTICS:
-->  150                     (A) LENGTH: 27 base pairs
151                          (B) TYPE: nucleic acid
152                          (C) STRANDEDNESS: single
153                          (D) TOPOLOGY: linear
154                (ii) MOLECULE TYPE: other nucleic acid
155                          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
156                                              GGGGTCTAGA CATCATCAAT A
```

```
157      (2) INFORMATION FOR SEQ ID NO:14:
158                (i) SEQUENCE CHARACTERISTICS:
-->  159                     (A) LENGTH: 32 base pairs
160                          (B) TYPE: nucleic acid
161                          (C) STRANDEDNESS: single
162                          (D) TOPOLOGY: linear
163                (ii) MOLECULE TYPE: other nucleic acid
164                          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
165                                              GGCGAATTCG TCGACAT
```

```
166      (2) INFORMATION FOR SEQ ID NO:15:
167                (i) SEQUENCE CHARACTERISTICS:
-->  168                     (A) LENGTH: 32 base pairs
169                          (B) TYPE: nucleic acid
170                          (C) STRANDEDNESS: single
171                          (D) TOPOLOGY: linear
172                (ii) MOLECULE TYPE: other nucleic acid
173                          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
174                                              GGCGAATTCG GTACCAT
```

```
175      (2) INFORMATION FOR SEQ ID NO:16:
176                (i) SEQUENCE CHARACTERISTICS:
-->  177                     (A) LENGTH: 17 base pairs
178                          (B) TYPE: nucleic acid
179                          (C) STRANDEDNESS: single
180                          (D) TOPOLOGY: linear
181                (ii) MOLECULE TYPE: other nucleic acid
182                          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
183                                              CTGTGTACAC CGGCGCA
```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 55 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
(ii)   MOLECULE TYPE: other nucleic acid

last cumulative total states "5620"

move over

CTTTCCTACT
TTGGCAGTAC
CCCCATTGAC

TCGTAACAAC TCCGCCCCAT TGACGCAAAT GGGCGGTAGG CGTGTACGGT GGGAGGTCTA

TATAAGCAGA
1080
1140
GGTCCCGGAT

TGACCTCCAT AGAAGACACC GGGACCGATC CAGCCTCCGG ACTCTAGAGG ATCCGGTACT
CGAGGAACTG AAAAACCAGA AAGTTAACTG GTAAGTTTAG TCTTTTTGTC TTTTATTTCA

CTTCTAGTAT CAAGCTTGAA TTCCTTTGTG TTACATTCTT GAATGTCGCT CGCAGTGACA
TTAGCATTCC GGTACTGTTG GTAAAATGGA AGACGCCAAA AACATAAAGA AAGGCCCGGC
GCCATTCTAT CCTCTAGAGG ATGGAACCGC TGGAGAGCAA CTGCATAAGG CTATGAAGAA
ATACGCCCTG GTTCCTGGAA CAATTGCTTT TACAGATGCA CATATCGAGG TGAACATCAC
GTACGCGGAA TACTTCGAAA TGTCCGTTCG GTTGGCAGAA GCTATGAAAC GATATGGGCT
GAATACAAAT CACAGAATCG TCGTATGCAG TGAAAACTCT CTTCAATTCT TTATGCCGGT
GTTGGGCGCG TTATTTATCG GAGTTGCAGT TGCGCCCGCG AACGACATTT ATAATGAACG
TGAATTGCTC AACAGTATGA ACATTTCGCA GCCTACCGTA GTGTTTGTTT CCAAAAAGGG
GTTGCAAAAA ATTTTGAACG TGCAAAAAAA ATTACCAATA ATCCAGAAAA TTATTATCAT

GGATTCTAAA
ACCTCCCGGT

TGCACTGATA ATGAATTCCT CTGGATCTAC TGGGTTACCT AAGGGTGTGG CCCTTCCGCA
TAGAACTGCC TGCGTCAGAT TCTCGCATGC CAGAGATCCT ATTTTTGGCA ATCAAATCAT
TCCGGATACT GCGATTTTAA GTGTTGTTCC ATTCCATCAC GGTTTTGGAA TGTTTACTAC
ACTCGGATAT TTGATATGTG GATTTCGAGT CGTCTTAATG TATAGATTTG AAGAAGAGCT
GTTTTTACGA TCCCTTCAGG ATTACAAAAT TCAAAGTGCG TTGCTAGTAC CAACCCTATT
TTCATTCTTC GCCAAAAGCA CTCTGATTGA CAAATACGAT TTATCTAATT TACACGAAAT
TGCTTCTGGG GGCGCACCTC TTTCGAAAGA AGTCGGGGAA GCGGTTGCAA AACGCTTCCA
TCTTCCAGGG ATACGACAAG GATATGGGCT CACTGAGACT ACATCAGCTA TTCTGATTAC
ACCCGAGGGG GATGATAAAC CGGGCGCGGT CGGTAAAGTT GTTCCATTTT TTGAAGCGAA
GGTTGTGGAT CTGGATACCG GGAAAACGCT GGGCGTTAAT CAGAGAGGCG AATTATGTGT
CAGAGGACCT ATGATTATGT CCGGTTATGT AAACAATCCG GAAGCGACCA ACGCCTTGAT
TGACAAGGAT GGATGGCTAC ATTCTGGAGA CATAGCTTAC TGGGACGAAG ACGAACACTT
CTTCATAGTT GACCGCTTGA AGTCTTTAAT TAAATACAAA GGATATCAGG TGGCCCCCGC
TGAATTGGAA TCGATATTGT TACAACACCC CAACATCTTC GACGCGGGCG TGGCAGGTCT
TCCCGACGAT GACGCCGGTG AACTTCCCGC CGCCGTTGTT GTTTTGGAGC ACGGAAAGAC
GATGACGGAA AAAGAGATCG TGGATTACGT CGCCAGTCAA GTAACAACCG CGAAAAAGTT
GCGCGGAGGA GTTGTGTTTG TGGACGAAGT ACCGAAAGGT CTTACCGGAA AACTCGACGC
AAGAAAAATC AGAGAGATCC TCATAAAGGC CAAGAAGGGC GGAAAGTCCA AATTGTAAAA
TGTAACTGTA TTCAGCGATG ACGAAATTCT TAGCTATTGT AATGGGGGAT CCCCAACTTG
TTTATTGCAG CTTATAATGG TTACAAATAA AGCAATAGCA TCACAAATTT CACAAATAAA
GCATTTTTTT CACTGCATTC TAGTTGTGGT TTGTCCAAAC TCATCAATGT ATCTTATCAT
GTCTGGATCG GATCGATCCC CGGGTACCGA GCTCGAATTC GTAATCATGG TCATAGCTGT
TTCCTGTGTG AAATTGTTAT CCGCTCACAA TTCCACACAA CATACGAGCC GGAAGCATAA
AGTGTAAAGC CTGGGGTGCC TAATGAGTGA GCTAACTCAC ATTAATTGCG TTGCGCTCAC
TGCCCGCTTT CCAGTCGGGA AACCTGTCGT GCCAGCTGCA TTAATGAATC GGCCAACGCG
CGGGGAGAGG CGGTTTGCGT ATTGGGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC
GCTCGGTCGT TCGGCTGCGG CGAGCGGTAT CAGCTCACTC AAAGGCGGTA ATACGGTTAT
CCACAGAATC AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG CAAAAGGCCA
GGAACCGTAA AAAGGCCGCG TTGCTGGCGT TTTTCCATAG GCTCCGCCCC CCTGACGAGC
ATCACAAAAA TCGACGCTCA GTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC
AGGCGTTTCC CCCTGGAAGC TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG
GATACCTGTC CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCATAGC TCACGCTGTA
GGTATCTCAG TTCGGTGTAG GTCGTTCGCT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG
TTCAGCCCGA CCGCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC

all text and cumulative base totals need to be visible on page

```
ACGACTTATC GCCACTGGCA GCAGCCACTG GTAACAGGAT TAGCAGAGCG AGGTATGTAG
GCGGTGCTAC AGAGTTCTTG AAGTGGTGGC CTAACTACGG CTACACTAGA AGGACAGTAT
TTGGTATCTG CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT
CCGGCAAACA AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG CAGATTACGC
GCAGAAAAAA AGGATCTCAA GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT
GGAACGAAAA CTCACGTTAA GGGATTTTGG TCATGAGATT ATCAAAAAGG ATCTTCACCT
AGATCCTTTT AAATTAAAAA TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT
GGTCTGACAG TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTC
GTTCATCCAT AGTTGCCTGA CTCCCCGTCG TGTAGATAAC TACGATACGG GAGGGCTTAC
CATCTGGCCC CAGTGCTGCA ATGATACCGC GAGACCCACG CTCACCGGCT CCAGATTTAT
CAGCAATAAA CCAGCCAGCC GGAAGGGCCG AGCGCAGAAG TGGTCCTGCA ACTTTATCCG
CCTCCATCCA GTCTATTAAT TGTTTGCCGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA
GTTTGCGCAA CGTTGTTGCC ATTGCTACAG GCATCGTGGT GTCACGCTCG TCGTTTGGTA
TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC CCCATGTTGT
GCAAAAAAGC GGTTAGCTCC TTCGGTCCTC CGATCGTTGT CAGAAGTAAG TTGGCCGCAG
TGTTATCACT CATGGTTATG GCAGCACTGC ATAATTCTCT TACTGTCATG CCATCCGTAA
GATGCTTTTC TGTGACTGGT GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC
GACCGAGTTG CTCTTGCCCG GCGTCAATAC GGGATAATAC CGCGCCACAT AGCAGAACTT
TAAAAGTGCT CATCATTGGA AAACGTTCTT CGGGGCGAAA ACTCTCAAGG ATCTTACCGC
TGTTGAGATC CAGTTCGATG TAACCCACTC GTGCACCCAA CTGATCTTCA GCATCTTTTA
CTTTCACCAG CGTTTCTGGG TGAGCAAAAA CAGGAAGGCA AAATGCCGCA AAAAAGGGAA
TAAGGGCGAC ACGGAAATGT TGAATACTCA TACTCTTCCT TTTTCAATAT TATTGAAGCA
TTTATCAGGG TTATTGTCTC ATGAGCGGAT ACATATTTGA ATGTATTTAG AAAAATAAAC
AAATAGGGGT TCCGCGCACA TTTCCCCGAA AAGTGCCACC TGACGTCTAA GAAACCATTA
TTATCATGAC ATTAACCTAT AAAAATAGGC GTATCACGAG GCCTATGCGG TGTGAAATAG
CGCACAGATG CGTAAGGAGA AAATACCGCA TCAGGCGCCA TTCGCCATTC AGGCTGCGCA
ACTGTTGGGA AGGGCGATCG GTGCGGGCCT CTTCGCTATT ACGCCAGCTG GCGAAAGGGG
GATGTGCTGC AAGGCGATTA AGTTGGGTAA CGCCAGGGTT TTCCCAGTCA CGACGTTGTA
                                                          AAACGACGGC CAGTGCC
```

(2) INFORMATION FOR SEQ ID NO:22:

      (i)   SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 45 base pairs

          (B) TYPE: nucleic acid

          (C) STRANDEDNESS: both

          (D) TOPOLOGY: linear

      (ii)   MOLECULE TYPE: other nucleic acid

      (iii)   HYPOTHETICAL: YES

      (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTACACTGAC CTAGTGCCGC CCGGGCAAAG CCCOOGCGGC ACTAG   45

[handwritten annotations:]

Seq 20 and 21 missing

what is this? These are invalid nucleic acid designators, per 1.822 (b) of Sequence Rules.

Please ensure: 1) all (A) LENGTH responses reflect actual number of bases 2) all bases are valid nucleic acid designators, per 1.822 (b) of Sequence Rules.